

## Appendix A

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2004, 08:34:06 ; Search time 2 Seconds  
(without alignments)  
3.960 Million cell updates/sec

Title: us-09-997-857-401  
Perfect score: 993  
Sequence: 1 MPVPALCLILWALWTRPAS.....AQOHLRQIQERLHTALPA 198

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 45 seqs, 40002 residues

Total number of hits satisfying chosen parameters: 45

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : rai.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	865	87.1	191	1	US-09-369-247-65
2					Sequence 65, Appl

## ALIGNMENTS

RESULT 1  
US-09-369-247-65  
; Sequence 65, Application US/09369247  
; Patent No. 6569992  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 44 Human Secreted Proteins  
; FILE REFERENCE: P2024P1  
; CURRENT APPLICATION NUMBER: US/09/369,247  
; CURRENT FILING DATE: 1999-08-05  
; EARLIER APPLICATION NUMBER: 60/074,118  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,157  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,137  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,341  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,141  
; EARLIER FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 65  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (25)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (191)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-369-247-65

Query Match 87.1%; Score 865; DB 1; Length 191;  
Best Local Similarity 93.2%; Pred. No. 2.3e-83;  
Matches 177; Conservative 1; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MPVPALCLILWALWTRPASAPMGPELAQOHLRQIQERLHTALPA 198  
DB 1 MPVPALCLILWALWTRPASAPMGPELAQOHLRQIQERLHTALPA 198  
QY 61 TKARNSLGLYGRTEILLGQEVSRGDAQAQELRASLLETQMEEDILQLOAEATAEVLGEVA 120  
DB 61 TKARNSLGLYGRTEILLGQEVSRGDAQAQELRASLLETQMEEDILQLOAEATAEVLGEVA 120  
QY 121 QAOQVLRDSVQRLVQLRSAMWGPAYREFVLRKAHADKQSHLWALTGHVQORREWVAQ 180  
DB 121 QAOQVLRDSVQRLVQLRSAMWGPAYREFVLRKAHADKQSHLWALTGHVQORREWVAQ 180  
QY 181 QHRLRQIQER 190  
DB 181 QHRLRQIQER 190